

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of the claims in the application.

LISTING OF CLAIMS:

1-87. Canceled.

88. (New) A method of tracking the spread of infectious bacteria, comprising:

- obtaining a plurality of bacterium samples from a plurality of patients or objects at a plurality of different physical locations;
- performing DNA sequencing on a first region of deoxyribonucleic acid from each bacterium sample, the first region consisting essentially of a variable number of tandem repeats (VNTRs) region;
- storing in a database for each of the plurality of bacterium samples: a) the nucleotide sequence data from the first sequenced region of each bacterium sample, and b) the physical location of the patient or object from which each bacterium sample was obtained;
- comparing the nucleotide sequence data stored in the database of at least two of the plurality of samples on both a base pair level and a repeat motif level;
- determining a measure of phylogenetic relatedness between the compared samples based upon differences between the compared nucleotide sequence data;
- identifying patients infected or objects contaminated with phylogenetically related bacteria based on the phylogenetic relatedness determination;
- tracking the spread over time of the bacteria based on: a) the identified patients or contaminated objects, and b) the physical locations of the identified patients or objects stored in the database; and
- providing a warning based on the tracking of the spread of the bacteria wherein the warning allows the recipient of the warning to control the further spread of the bacteria, and further wherein said region consisting essentially of a variable number of tandem repeats (VNTRs) comprise at least one sequence selected from the

group consisting of SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:78, SEQ ID NO:79, and SEQ ID NO:80.

89. (New) The method of Claim 88, wherein the at least one point mutation is not in the first three nucleotides of the at least one sequence.
90. (New) The method of Claim 88, wherein the first three nucleotides of the at least one sequence are GAT or GAC.
91. (New) The method of Claim 88, wherein said region consisting essentially of a variable number of tandem repeats (VNTRs) comprises more than one sequence selected from the group consisting of SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:78, SEQ ID NO:79, and SEQ ID NO:80.
92. (New) The method of Claim 88, wherein the deoxyribonucleic acid sequence from each bacterium sample is compared against SEQ ID NO:54.
93. (New) The method of Claim 88, wherein the database is a centralized database located at a different location from where the sample is obtained.

94. (New) The method of Claim 88, wherein the database is located in the same location as where the sample is obtained.
95. (New) The method of Claim 88, wherein each bacterium sample is obtained from a patient as the patient is admitted to a health care facility and prior to being exposed to patients in the health care facility.
96. (New) The method of Claim 88, further comprising:
obtaining a medical history from a patient from which at least one
of the plurality of bacterium samples was taken;
determining an infection risk factor based on the patient's medical
history, the infection risk factor being a measure of the patient's
risk of acquiring an infection; and
taking appropriate infection control measures in accordance with the
infection risk factor.
97. (New) The method of Claim 88, further comprising:
segregating the information contained within the patient's medical
history into private information and non-private information;
transmitting the patient's non-private information to the database
without transmitting the patient's private information; and
storing the patient's private information in a database at a different
location from the database to which the patient's non-private
information is transmitted.

98. (New) The method of Claim 88, wherein the step of performing DNA sequencing comprises either:
- sequencing the first region at a physically separate facility and transmitting the resulting nucleotide sequence data to the database via a computer network; or
 - sending each of the plurality of bacterium samples to an infection control facility that has access to the database, sequencing the first region at the infection control facility, and storing the nucleotide sequence data in the database.
99. (New) The method of Claim 88, wherein the first region is identified by a set of primers.
100. (New) The method of Claim 99, wherein said primers are selected from the group consisting of SEQ ID NO:75, SEQ ID NO:76, and SEQ ID NO:77.
101. (New) The method of Claim 88, wherein the first region is amplified prior to DNA sequencing.
102. (New) The method of Claim 88, wherein the step of determining the phylogenetic relatedness between at least two compared samples comprises:
- identifying repeat sequences in the nucleotide sequence data from each sample;
 - and
 - treating the insertion or deletion of a repeat sequence as a single genetic event.
103. (New) The method of Claim 88, wherein the step of determining the phylogenetic relatedness between at least two compared samples comprises:
- identifying individual single nucleotide polymorphisms in the nucleotide sequence data from each sample; and
 - treating an insertion or deletion or change of an individual nucleotide as a single genetic event.

104. (New) The method of Claim 88, wherein the step of determining the phylogenetic relatedness between at least two compared samples comprises at least one of:
- comparing a first bacterium sample to other samples obtained from the same location as where the first bacterium sample was taken, thereby determining a local phylogenetic relatedness;
 - comparing the first bacterium sample to other samples obtained from the same geographical region as where the first bacterium sample was taken, thereby determining a regional phylogenetic relatedness; and
 - comparing the first bacterium sample to other samples obtained globally, thereby determining a global phylogenetic relatedness.
105. (New) The method of Claim 88, wherein the steps of storing nucleotide sequence data in a database and tracking the spread of the infection further comprises:
- transmitting over a computer network the nucleotide sequence data from the first sequenced region of each of the plurality of bacterium samples and the physical location of the patient or object from which each bacterium sample is taken.
106. (New) The method of Claim 105, further comprising:
- storing in the database a map of the physical location of where the plurality of samples were obtained; and
 - determining the spread of the infection based on the map.
107. (New) The method of Claim 106, further comprising:
- determining, via sensor, the patient's physical location prior to transmitting the patient's physical location.
108. (New) The method of Claim 88, further comprising:
- determining the virulence of the bacterium by retrieving the virulence data of identical or similar bacteria from the database; and
 - transmitting over a computer network virulence information to a location where the bacterium sample was obtained.

109. (New) The method of Claim 88, further comprising:
determining drug resistance and treatment information of the bacterium
by retrieving drug information data of identical or similar
bacteria from the database; and
transmitting over a computer network the drug information data to a
location where the bacterium sample was obtained.
110. (New) The method of Claim 88, wherein providing a warning comprises:
determining whether a location where each bacterium was
obtained has an outbreak problem; and
transmitting over a computer network an outbreak warning to each
location having an outbreak problem.
111. (New) The method of Claim 88, further comprising:
performing DNA sequencing on a second region of deoxyribonucleic
acid of each bacterium sample;
storing the nucleotide sequence data from the second region of the
deoxyribonucleic acid of each bacterium sample in a database;
comparing the nucleotide sequence data from the second
sequenced region to nucleotide sequence data already
stored in the database; and
determining a measure of phylogenetic relatedness based on the
comparison of the first and second sequenced regions.
112. (New) The method of Claim 111, wherein the determination of relatedness based on
the second sequenced region is used to verify the determination of relatedness based on
the first sequenced region.
113. (New) The method of Claim 111, further comprising:
identifying a first level of subspecies of each bacterium sample
based on the first sequenced region; and
identifying a second level of subspecies of each bacterium sample
based on the second sequenced region.

114. (New) The method of Claim 111, further comprising:

tracking the global spread of an infection based on the sequencing and
comparing a slowly mutating region of the deoxyribonucleic
acid; and

tracking the local spread of an infection based on the sequencing and
comparing a more rapidly mutating region of the
deoxyribonucleic acid.

115. (New) A system for tracking the spread of infectious bacteria, comprising:

a computer network;

a centralized database;

a facility, connected to the computer network, where a plurality of
bacterium samples from a plurality of patients or objects at a
plurality of different locations are obtained;

a server connected to the computer network, the server receiving
nucleotide sequence data for a first sequenced region of a
deoxyribonucleic acid from each of the plurality of bacterium
samples and a physical location of a patient or object from which
each bacterium sample was obtained, the first sequenced region
consisting essentially of a variable number of tandem
repeats (VNTRs) region;

storing in a database for each of the plurality of bacterium samples: a)
the nucleotide sequence data from each of the plurality of
bacterium samples, and b) the physical location of the patient or
object from which each bacterium sample was obtained;

accessing the centralized database and comparing the stored nucleotide
sequence data of at least two of the plurality of bacterium
samples;

determining a measure of phylogenetic relatedness between the
compared samples;

identifying patients infected or objects contaminated with
phylogenetically related bacteria based on the phylogenetic
relatedness determination;

tracking the spread over time of the bacteria based on a) the identified patients or objects, and b) and the physical locations of the identified patients or objects stored in the database; and transmitting a warning over the computer network to the facility based on the tracking of the spread of the bacteria, thereby allowing the facility to control further spread of the bacterial infection, wherein said region consisting essentially of a variable number of tandem repeats (VNTRs) comprise at least one sequence selected from the group consisting of SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:78, SEQ ID NO:79, and SEQ ID NO:80.

116. (New) Computer-executable software code stored on a computer-readable medium for performing the method according to Claim 88, wherein said spread of infectious bacteria is tracked using a computer network.
117. (New) The method of Claim 88, wherein the plurality of bacterium samples are obtained at a location physically separate from where the DNA sequencing is performed.
118. (New) The method of Claim 117, wherein the physically separate location is a health care facility, and the sample of the bacterium is obtained from a patient as the patient is admitted to a health care facility and prior to being exposed to patients in the health care facility.
119. (New) The method of Claim 88, wherein the sample is obtained at a location physically separate from where the DNA sequencing, comparing, and determination of a measure of phylogenetic relatedness occurs.
120. (New) The method of Claim 88, wherein what may be an outbreak of bacterial infection is confirmed or refuted based upon the determination of phylogenetic relatedness.

121. (New) The system of Claim 115, wherein the DNA sequencing occurs at the facility and further wherein the nucleotide sequence data is transmitted over the computer network to the server.
122. (New) The system of Claim 115, wherein the step of determining the phylogenetic relatedness between at least two compared samples comprises:
 - identifying repeat sequences in the nucleotide sequence data from each sample;
 - and
 - treating the insertion or deletion of a repeat sequence as a single genetic event.
123. (New) The system of Claim 115, wherein the step of determining the phylogenetic relatedness between at least two compared samples comprises:
 - identifying individual single nucleotide polymorphisms in the nucleotide sequence data from each sample; and
 - treating the insertion or deletion or change of an individual nucleotide as a single genetic event.